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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=22; hr=9; min=26; sec=4; ms=670;]

=====

Reviewer Comments:

<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES

<130> P89103PWO

<140> 10511130

<141> 2005-08-15

<150> PCT/GB2003/001623

<151> 2003-04-15

<160> 32

Numeric identifier <160> must reflect the total number of sequences found in the sequence listing. This file contains 33 SEQ ID numbers, but <160> states there are 32. Please make all necessary changes.

<210> 13

<211> 103

<212> PRT

<213> RB69

* * * * *

Numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." Please make all necessary changes.

<210> 33
<211> 13
<212> PRT
<213> Unknown
<220>
<223> amino acid motif where X can be any amino acid

<400> 33

Glu Xaa Xaa Ile Xaa Phe/Tyr Xaa Xaa Xaa Tyr Xaa Xaa Asp
1 5 10

Numeric identifier <211> must reflect the total number of amino acids in the sequence. <211> states there are 13 amino acids in SEQ ID # 33, but the actual count is 14. Please make all necessary changes.

A sequence cannot contain any non-sequence related symbols. Please remove "/" from SEQ ID # 33.

Application No: 10511130 Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144
Finished: 2008-09-20 06:22:44.841
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms
Total Warnings: 23
Total Errors: 2
No. of SeqIDs Defined: 32
Actual SeqID Count: 33

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)

Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144
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Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms
Total Warnings: 23
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No. of SeqIDs Defined: 32
Actual SeqID Count: 33

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
E 330	Invalid protein , found in SEQID(33) POS (6)Invalid
W 333	tabs used in amino acid numbering SEQID (33)
E 252	Calc# of Seq. differs from actual; 32 seqIds defined; count=33

SEQUENCE LISTING

<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES

<130> P89103PWO

<140> 10511130

<141> 2005-08-15

<150> PCT/GB2003/001623

<151> 2003-04-15

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 776

<212> PRT

<213> Unknown

<220>

<223> Variant derived from Pyrococcus furiosus Pfu-Polymerase

<400> 1

Met Ala Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val

1

5

10

15

Ile Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp
20 25 30

Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys
35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val
50 55 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro
65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
100 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile
115 120 125

Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu
130 135 140

Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met
145 150 155 160

Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn
165 170 175

Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile
180 185 190

Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val
195 200 205

Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala
210 215 220

Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro
225 230 235 240

Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg		
245	250	255
Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro		
260	265	270
Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys		
275	280	285
Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu		
290	295	300
Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr		
305	310	315 320
Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg		
325	330	335
Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn		
340	345	350
Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val		
355	360	365
Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu		
370	375	380
Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu		
385	390	395 400
Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile		
405	410	415
Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn		
420	425	430
Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro		
435	440	445
Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys		
450	455	460

Ile Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu
465 470 475 480

Leu Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr
485 490 495

Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala
500 505 510

Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys
515 520 525

Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp
530 535 540

Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys
545 550 555 560

Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu
565 570 575

Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr
580 585 590

Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg
595 600 605

Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr
610 615 620

Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu
625 630 635 640

Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu
645 650 655

Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu
660 665 670

His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu
675 680 685

Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile

690

695

700

Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu
705 710 715 720

Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu
725 730 735

Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr
740 745 750

Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr
755 760 765

Ser Trp Leu Asn Ile Lys Lys Ser
770 775

<210> 2

<211> 775

<212> PRT

<213> *Pyrococcus furiosus*

<400> 2

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320

Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu	325	330	335	
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350	
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala	355	360	365	
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380	
Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn	385	390	395	400
Ile	Val	Tyr	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415	
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Leu	Glu	Gly	Cys	Lys	Asn	Tyr	420	425	430	
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly	435	440	445	
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile	450	455	460	
Lys	Thr	Lys	Met	Lys	Glu	Thr	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	465	470	475	480
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	485	490	495	
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505	510	
Ser	Val	Thr	Ala	Trp	Gly	Arg	Lys	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu	515	520	525	
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	530	535	540	

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625 630 635 640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
755 760 765

Trp Leu Asn Ile Lys Lys Ser

770

775

<210> 3

<211> 776

<212> PRT

<213> Unknown

<220>

<223> Variant derived from *Pyrococcus furiosus* Pfu-Polymerase

<400> 3

Met Ala Ile Leu Asp Val Asp Ala Ile Thr Glu Glu Gly Lys Pro Val
1 5 10 15

Ile Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp
20 25 30

Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys
35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val
50 55 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro
65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
100 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile
115 120 125

Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu
130 135 140

Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met
145 150 155 160

Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn
165 170 175

Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile
180 185 190

Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val
195 200 205

Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala
210 215 220

Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro
225 230 235 240

Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg
245 250 255

Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro
260 265 270

Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys
275 280 285

Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu
290 295 300

Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr
305 310 315 320

Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg
325 330 335

Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn
340 345 350

Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val
355 360 365

Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu
370 375 380

Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu
385 390 395 400

Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile
405 410 415

Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn
420 425 430

Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro
435 440 445

Gly Phe Ile Pro Ser Leu Leu Gly His Leu L